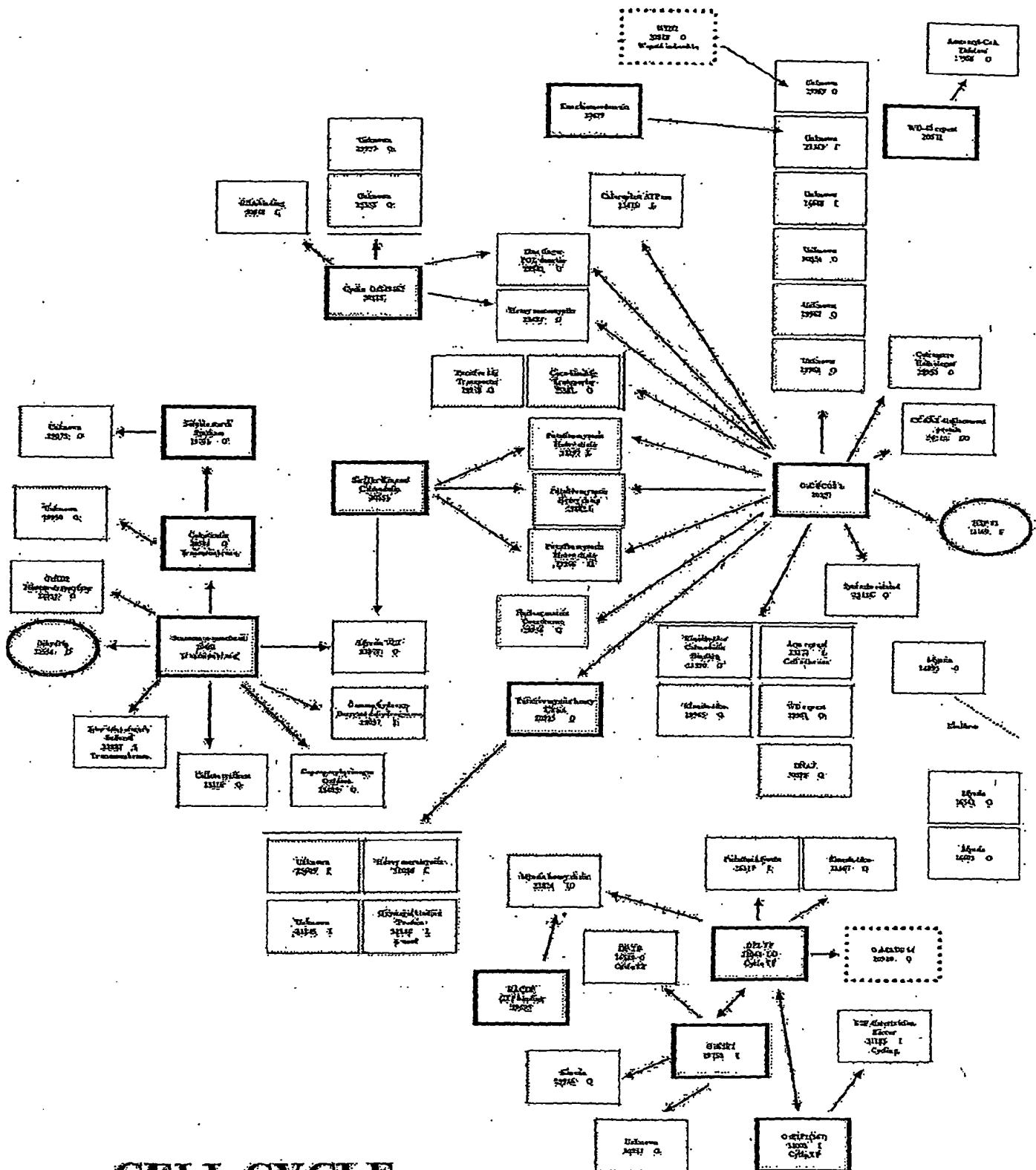


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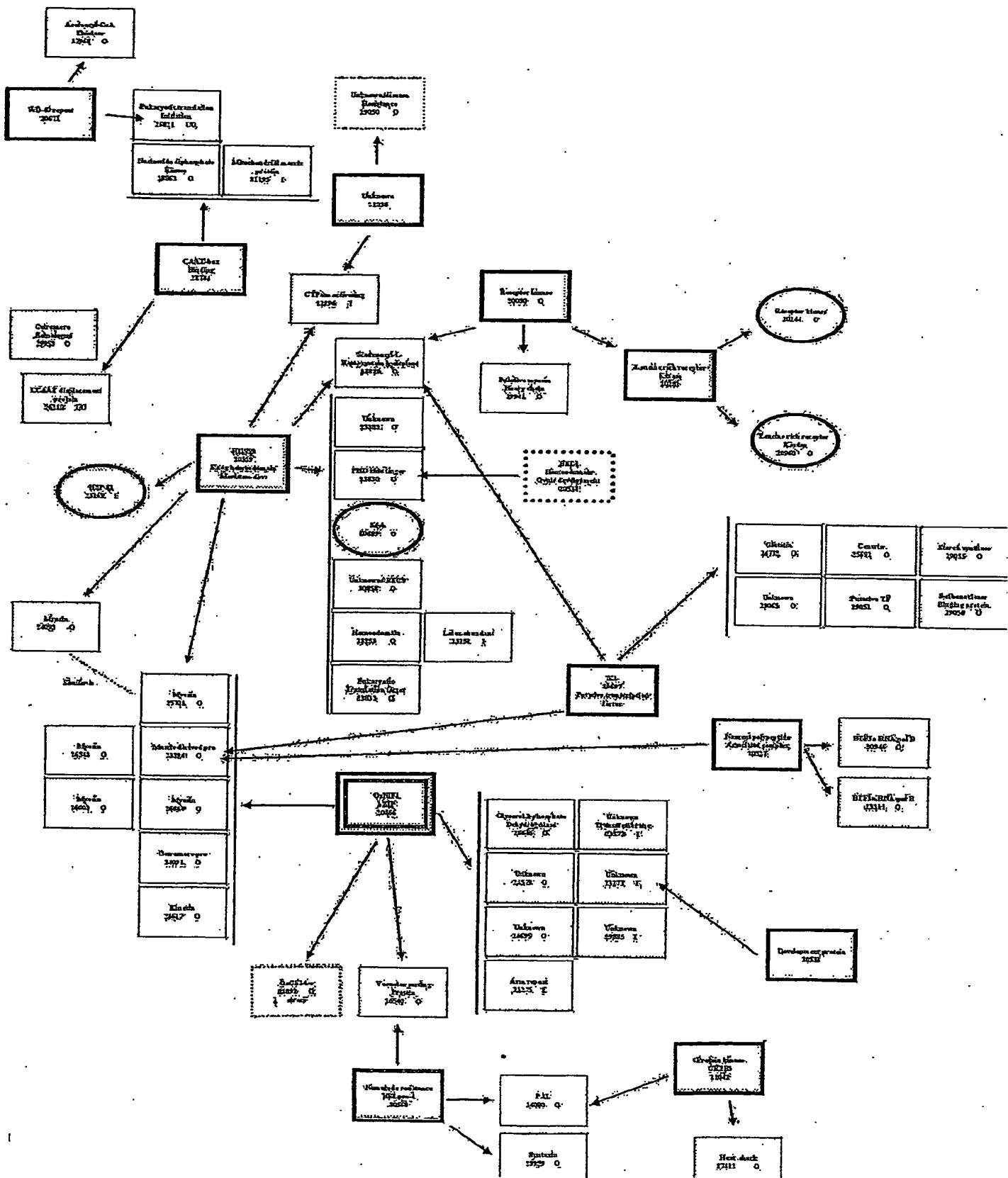
FIGURE 1A



CELL CYCLE

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FIGURE 1B



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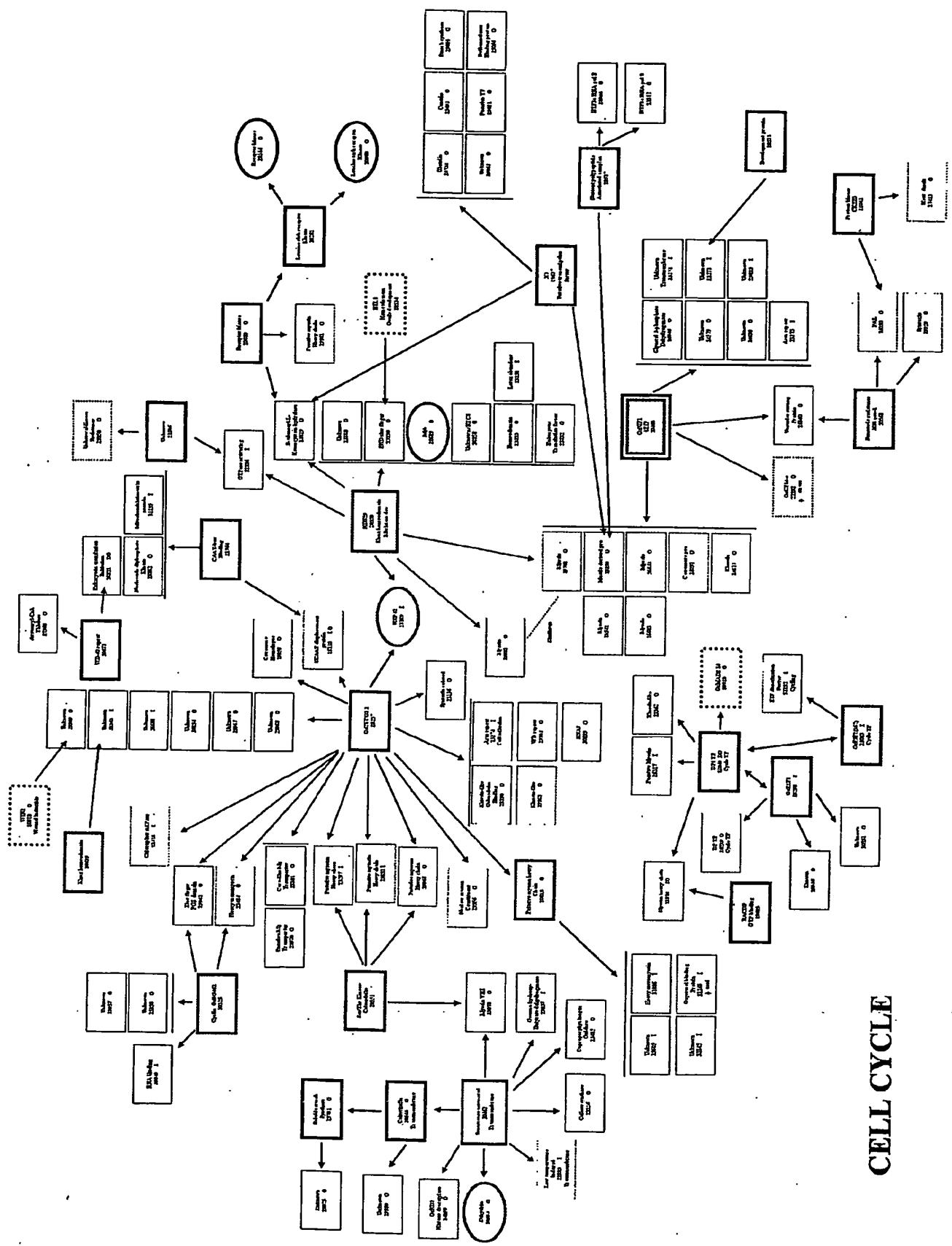
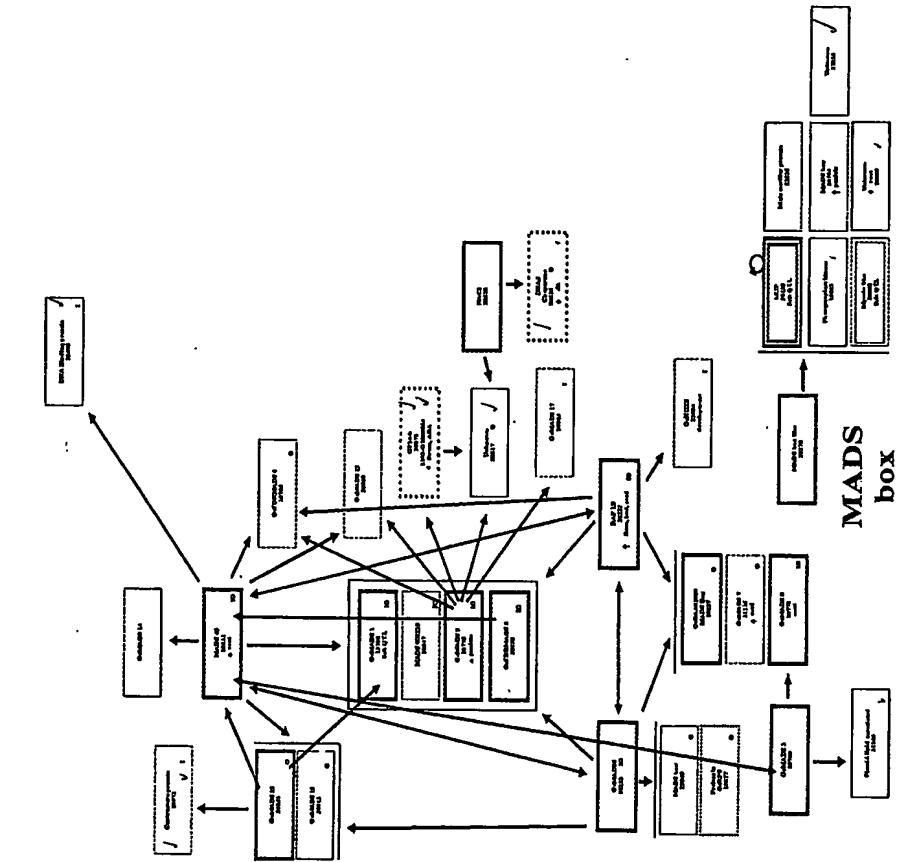


FIGURE 1C



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19766	OLEKQLESSLKHIRSRSRKTQLLEQISELQRKEKSLOQUEENKVLOQKKLVETEK--	--GQQVQQQG-WDQQGQTPA
19788	QLEQQLENSLKHIRSRSRKSQMLSESINELQRKEKSLOQUEENKVLOQKELVEKQK-VQKQQ--	-VQWDQTQPQT
20231	SLEKOLDSSLKHVRTRTRTKHLVDQLTELQRKEQMVSSEANRCLRRKLEESNHVRQQVWEQGCNLLIGYER	
20232	QLEQQLENSLKHIRSRSRKSQMLSESINELQRKEKSLOQUEENKVLOQKELVEKQK-VQKQQ--	-AENTLHMSWQDGGS
20233	QLEKQLECALSQARQRKTQLMMEQVEELLRKEROLGEINRQLKHKLEVEGSTSNYRAMQQASWAQG---	
20278	GIEFQNVDAAALKEVHRKIHVITIQTETYKKVKHSYEAYETLQQELGLREEPAFGFVDNTGGWDG---	
20668	QLESRLEKGIAKIRAKRNELLASEINTMAKREIELQNDMMDLRTKIAEEQQLQQVTVARSAAMEL---	
20698	GLEMKLEKSLHNTRIKKTELLERQIAKLIKEKERTILKDNNENLRGKHMRNIEAAAIVANHMTTITAPAA---	
20700	QVENRLEKGIAKIRARKNELLIAEVEYMQKREVELQONDNMYLRSKVVENENERGQQPLNMGAAS-----	
20707	QLENQIEISLMNITRSKNOQOLIDQVFELKRKEQQLODANKDLKRKIQETS--GENMLHISCQDVG-PS	
20778	QLEKQDSSLRHIRSTRTQHMDQLTDLQRREQMLCEANKCLRRKLEESNQLHG-QVWEHGATLLGYER	
20837	QLEKNLEAGLHRVMLTKDQQFMEQISELQRKSSQLAEEENMQLRNQVSQISPAEKQVV--DTENFVTEGQ	
20842	QLEQQLESSLKHIIISRKSHLMI.EISISELQKKERSLQEENKALQKELVERQNKVRGQQQVQGWQDQTQVQA	
20847	ELEKSLESGLGSVLKITSKKKNQLLFEISELQKEKSLSKNQNNVQK-LMETEK--EKNNAIINTNREEQNG	
20910	QLEQQLENSLKHIRSRSRKSQMLSESINELQRKEKSLOQUEENKVLOQKELVEKQK-VQKQQ--	-VQWDQTQPQT
20912	QLEHQLEYSLKHRSKKNQLLFEISELQKEKSLSKNQNNVQK-LMETEK--EKNNAIINTNREEQNG	
20914	QLEKQLEYSLSQARQRKTQIMMEQVDDLRRKEROLGELNKQLKNNLEADSSNCRSAIQDSWVHG--	
21116	SLEKOLDSSLKHVRTRTRTKHLVDQLTELQRKEQMVSSEANRCLRRKLEESNHVRQQVWEQGCNLLIGYER	
22949	GLENRLEISLRNIRMKDNLLKSEIEELHVKGSLIHQENIEUSRSLNVMSOOQKLELYNKLOACEO-----	

FIGURE 3A

Cons.	-A-QQ-PPHSSS-F-HREAA-EPTLNIGY--AAGERIA-----Q-----LPP-WML-----
19766	--SSSSSSFMMREA--LPTTNISN-YPAAGER-----IEDVAAGQPQHVRIG-LPPWMLSHING-----
20910	--SSSSSSFMMREA--LPTTNISN-YPAAGER-----IEDVAAGQPQHHERIG-LPPWMLSHING-----
20232	--ISSSSSFMMREA--LPTTNISN-YPAAGER-----IEDVPAGQPQHVRIG-LPPWMLSHING-----
20842	QAQAQPQAAQTSSSSSMRLRQQALLPPQNICY-PPVMMGERNDAAAAVAAGQVQLRIGGLPPWMLRTSHT-----
20912	--ATPSTSSPPTPVTAPDPIPTTNNSQSPRGSCS-----EAQPSPAQAGNSKLPPWMLRTSHT-----
19788	GS-----STVLADOPPHHQGLLHPHDQGDHSLSLQIGYH-----RPH-AHHHQAYMDHLNSNEADMVAHHPNENHPSGWI-----
20770	G-----HASEANQEFLHHAICDP-----SLHIGY-----QAYMDHLNQ-----
20231	QP-----EVQQ-PLHGGNGFFHPLDAAGEPTLQIGY-----AEHHEAMNSACMTNTYMPFWLP-----
21116	QP-----EVQQ-PLHGGNGFFHPLDAAGEPTLQIGY-----AEHHEAMNSACMTNTYMPFWLP-----
20778	QSP-----HAVQQVPPHGNGFFHSLEAAAEPTLQIGFT-----PEQ---MNNSCYTAFMPTWLP-----
20233	--AVVENG-AAYVQPPPHSAAMDSEPTLQIGY-----HQFVPAEANTIQRSTAPAGAE-----NNFMLGWVL-----
20914	--TVVSGGRVNLNAQOPPPD--IDCEPTLQIGY-----YQFVRPEAANPRSNGGGDQN-----NNFVMGWPL-----
20698	--AWPRDVPMTSSTAGAADAMDVETDLYIGLP-----GTERSSNRSETG-----
20668	--QAAAAAQQQQQNPFAVAAQLDMKCFPLNLFEAAAQQVQAVAAQRQQIIPTEELNLYHHHLAIPGATAADAPPHF-----
20700	--TSEYDHMVNNPY-----DSRNFLQVNIMQ-----QPOHYAHQLQ-----PTTLQLGQOQAFN-----
29949	--RGATDANESSSTPY-----SFRIIIONANMPPSLELSQSQQREGECSKTAPELGLHLP-----
20278	--GAGAGAAAD-----MFAFRVVPSPQPNLHGMAYGGN-----HDRLG-----
20837	--SSESVMTALHSGSSQSQDDGSDVSLKLGLPCGAWK-----
20847	--SSESVTNASYP--RPPPDNDYSSDTSLKLGHS-----

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Cons.	
19766	-MGRGRVELKRIENKINRQVTGSKRRNGLLKKAYELSVLCDAEVALIIFSSRGKLYEFASSS
20910	-MGRGKVQLKRIENTINRQVTFSKRRSGLKKANEISVLCDAEVALIIFSTKGKLYEYATDS
20232	-MGRGKVQLKRIENKINRQVTFSKRRSGLKKANEISVLCDAEVALIIFSTKGKLYEYATDS
20842	-MGRGKVQLKRIENKINRQVTFSKRRSGLKKANEISVLCDAEVALIIFSTKGKLYEYATDS
20912	-MGRGPVQLRRIENKINRQVTESKRRNGLLKKAHESISVLCDAEVAIAIVSPKGKLYEYATDS
19788	-MGRGKVELKRIENKISRQVTFAKRRNGLLKKAYELSILLCDAEVALIIFSSGRGRLPEFSSSS
20770	-MGRGKVELKRIENKISRQVTFAKRRNGLLKKAYELSVLCDAEVALIIFSTRGRLPEFSTSS
20231	-MGRGRVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCDAEVALIIFSNRGKLYEFCSTQ
21116	LVGGSWRSIGMGRGRVELKRIENKINRQVTFAKRRNGLLKKAYELSILLCDAEVALIIFSSGRGRLPEFSSSS
20778	-MGRGRVELKRIENKINRQVTFAKRRNGLLKKAYELSVLCDAEVALIIFSNRGKLYEFCSGQ
20233	-MGRGRVELKRIENKINRQVTFSKRRNGLLKKAYELSVLCDAEVALIIFSSRGKLYEFGSAG
20914	-MGRGRVELKRIENKINRQVTFSKRRNGLLKKAYELSVLCDAEVALIIFSSRGKLYEFGSAG
20698	MV-----RGRTELKRIENPTSRQVTFSKRRNGLLKKAFELSVLCDAEVALIIVFSPRGRGLYEFASAP
20668	-MGRGRRIEIKRIENTTSRQVTFCKRRNGLLKKAYELSVLCDAEVALIIVFSSRGRLYEYNNNN
20700	-MGRGKIEIKRIENTINRQVTFCRKRRNGLLKKAYELSVLCDAEVALIIVFSSRGRLYEYANN-
2949	-MGRGKIVIRRIDNSTSRQVTFSKRRNGLLKKAKELSILICDAEVGLVVFSSTGXLYEFSSST-
20278	-MGRGKIEIKRIENATMRQVTYSKRRTGIMKKARELTIVLDAQVALIMFSSTGKYHEFCSPST
20837	MA-----RERREIKRIESAAARQVTFSKRRGLFKKAELSVLCDADVALIIVFSSTGKLSHFASSS-
20847	ESEG-----RAATGKERRIAIRRIDNLAARQVTFSKRRRGFLFKKAELLSILCDAEVGLVVFSATGKLFOFASTS-

FIGURE 3C

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Cons.	S-MTKTLLERYQRYSYA--ESSAVISAESSETQGSWYQEYLKLKAKVEALQKTQRH-----LLGEDLESLSLKELQ
19766	CMDKILLERYERYSYAEK--VLISAESDTQGNWCHEYRKLLKAKVETIQCQ-KHMGEDLESLNLKELQ
20910	CMDKILLERYERYSYAEK--VLISAESDTQGNWCHEYRKLLKAKVETIQCQ-KHMGEDLESLNLKELQ
20232	CMDKILLERYERYSYAEK--VLISAESDTQGNWCHEYRKLLKAKVETIQCQ-KHMGEDLESLNLKELQ
20842	RMDKILLERYERYSYAEK--ALISAESSESEGNCHEYRKLLKAKIETIQCCH-KHMGEDHESLNLKELQ
20912	SMEGILLERYQRYSPFDER--AVLEPNTEDQENWGDEYGLKSQDALKSQ-RQLLGEQLDTLTTKELQ
19788	CMYKTLLEERYRSCNYNS---QDAAPENEIN-YQEYLKLKTRVEFLQTTQ-RNLLGEDLGPLSMKEL
20770	CMYKTLLEERYRSCNYNLN-SCEASAALETELSNYQEYLKLKTRVEFLQTTQ-RNLLGEDLVPLSLKEL
20231	SMTKTLEKYQKCSYAGPETAVQNRESQLKASRNNEYLKLKARVENLQRTQ-RNLLGEDLGPLSMKEL
21116	SMTKTLEKYQKCSYAGPETAVQNRESQLKASRNNEYLKLKARVENLQRTQ-RNLLGPDLLSLGIKELE
20778	SMTRTLLERYQKFSYGGPDITQNKENELVQSSRNNEYLKLKARVENLQRTQ-RNLLGEDLGTLLGIKELE
20233	-ITKTLERYQHCCYNAQ-DSNNALS--ETQSWYHEMSKLKAKFEALQRTQ-RHLLGEDLGPLSVKELQ
20914	-INKTLEKYNSSCCYNAQ-GSNSALAGGEHQSWYQEMSRILKTKLECLQRSQ-RHMLGEDLGPLSIKELE
20698	SLOQTIDRYKAYTKDHV--NNKTIQDIOQQVKDDTGLAKKLEALDESR-RKILGENLEGCSIEELR
20668	NVKATIDRYKKAHAACGSTSGAPLIEVNAQYYQQESAKLRHQIOMLQNTN-KHLVGDNVNLSLKELK
20700	SVKSTVERYKKANSDTNSGGT-VAEVNAQHY-QESESSKLRQQISSLQNANSRTIVGDSINTMSLRLK
29949	NMKTVIDRYTNAKEELLGGNA----TSEIJKIWQREAASLRQQLHNLQESH-KQLMGEELSGLGVRDLQ
20278	DIKGIFDRYQQAIGTS-----LWIEQYENMVRTLSHLDINRNLRTEI-RQRMGEDLGLEFDELR
20837	-MNEIIDKYNTHSNNLG--KAEQPSLDLNLEHS-KYAHINEQLAESLRL-RQMRGEELLEGLSIDELO
20847	-MEQIIDDRYNSHSKTLQ--RAEPSQLDQGEDSSTCARIKEELAETSLRL-RQMRGEELHRLNVEQLQ

FIGURE 3D

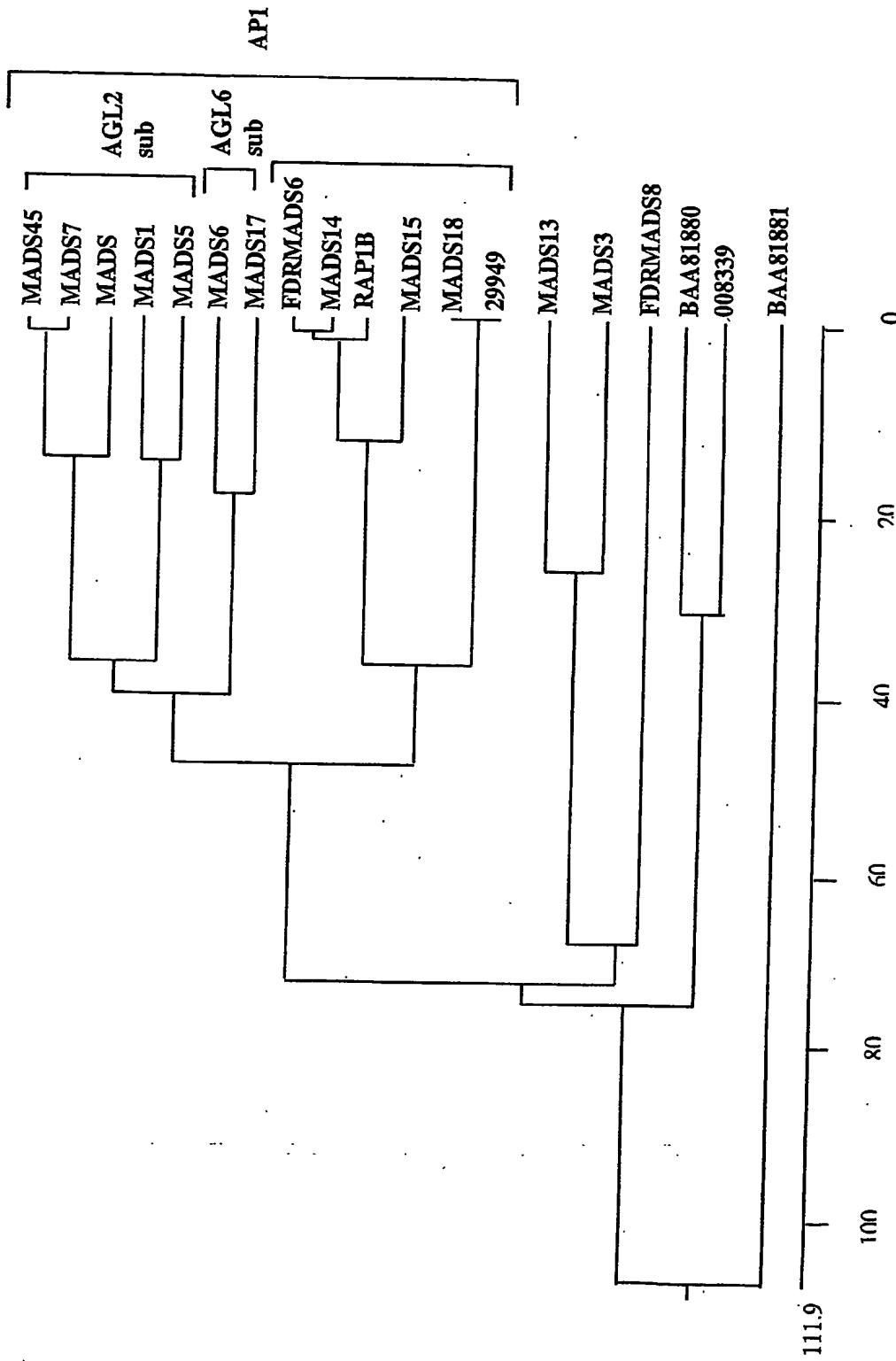
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FIGURE 3E



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Fig. 4

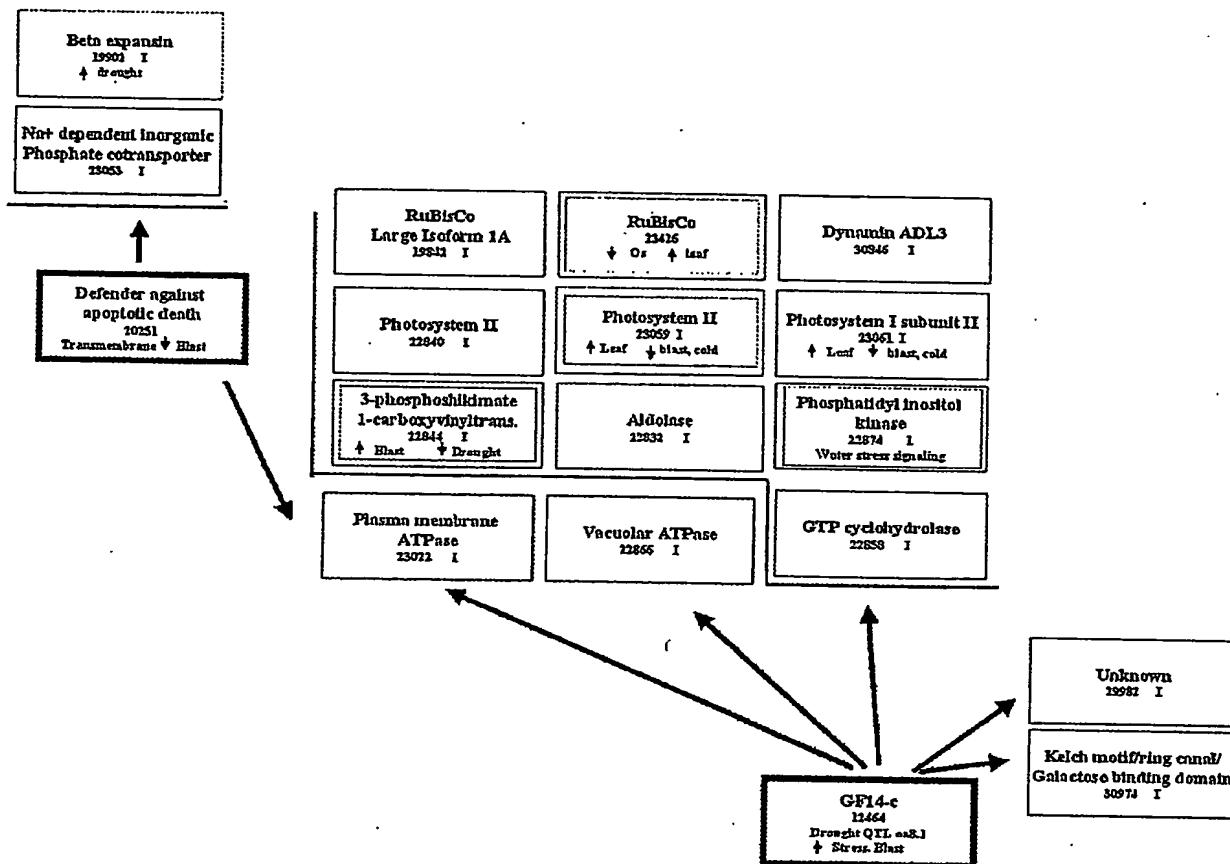
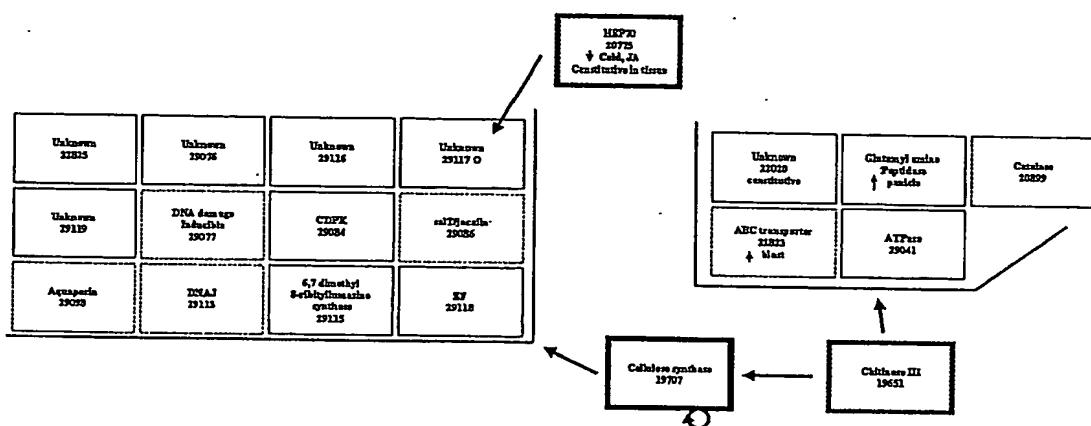


Fig. 5

CHITINASE AND CELLULOSE SYNTHASE INTERACTIONS



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Fig. 6

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